BIOTECHNOLOGY
SYSTEMS
BRANCH

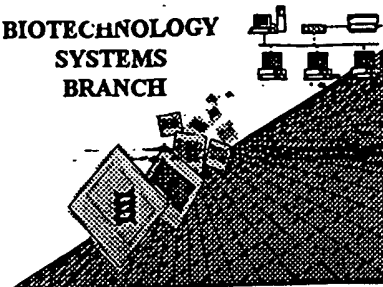# RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/669,187_

Source: _OIPE_

Date Processed by STIC: _10-03-00_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,

2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR FURTHER INFORMATION, PLEASE TELEPHONE MARK SPENCER, 703-308-4212.

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER VERSION 3.0 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).
Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

<u>Checker Version 3.0 can be down loaded from the USPTO website at the following address:</u>
http://www.uspto.gov/web/offices/pac/checker

●Raw Sequence Listing Error Summary

ERROR DETECTED   SUGGESTED   CORRECTION   SERIAL NUMBER: _09/669,187_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics

The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 _____ Wrapped Aminos

The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 _____ Incorrect Line Length

The rules require that a line not exceed 72 characters in length. This includes spaces.

4 _____ Misaligned Amino Acid Numbering

The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 _____ Non-ASCII

This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 _____ Variable Length

Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.

7 _____ PatentIn ver. 2.0 "bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) _____. Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence. **This applies primarily to the mandatory <220>-<223>
sections for Artificial or Unknown sequences.**

8 _____ Skipped Sequences (OLD RULES)

Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 _____ Skipped Sequences (NEW RULES)

Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

10 _____ Use of n's or Xaa's (NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 _____ Use of <213>Organism (NEW RULES)

Sequence(s) _____ are missing this mandatory field or its response.

12 _✓_ Use of <220>Feature (NEW RULES)

Sequence(s) _____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of new Rules)

13 _____ PatentIn ver. 2.0 "bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/669,187

DATE: 10/03/2000
TIME: 15:21:53

Input Set : A:\C10397035US.txt
Output Set: N:\CRF3\10032000\I669187.raw

```
       4 <110> APPLICANT: Krieg, Arthur M.
       5        Schetter, Christian
       6        Vollmer, Jorg
       9 <120> TITLE OF INVENTION: Immunostimulatory Nucleic Acids
      11 <130> FILE REFERENCE: C1039/7035 (HCL/MAT)
C--> 13 <140> CURRENT APPLICATION NUMBER: US/09/669,187
C--> 13 <141> CURRENT FILING DATE: 2000-09-25
      13 <150> PRIOR APPLICATION NUMBER: US 60/156,113
      14 <151> PRIOR FILING DATE: 1999-09-25
      16 <150> PRIOR APPLICATION NUMBER: US 60/156,135
      17 <151> PRIOR FILING DATE: 1999-09-27
      19 <150> PRIOR APPLICATION NUMBER: US 60/227,436
      20 <151> PRIOR FILING DATE: 2000-08-23
      22 <160> NUMBER OF SEQ ID NOS: 1145
      24 <170> SOFTWARE: FastSEQ for Windows Version 3.0
      26 <210> SEQ ID NO: 1
      27 <211> LENGTH: 18
      28 <212> TYPE: DNA
      29 <213> ORGANISM: Artificial Sequence
      31 <220> FEATURE:
      32 <223> OTHER INFORMATION: Synthetic Sequence
      34 <400> SEQUENCE: 1                                     18
      35  tctcccagcg tgcgccat
      37 <210> SEQ ID NO: 2
      38 <211> LENGTH: 20
      39 <212> TYPE: DNA
      40 <213> ORGANISM: Artificial Sequence
W--> 42 <220> FEATURE:
W--> 42 <223> OTHER INFORMATION:
      42 <400> SEQUENCE: 2                                     20
      43  ataatccagc ttgaaccaag
      45 <210> SEQ ID NO: 3
      46 <211> LENGTH: 20
      47 <212> TYPE: DNA
      48 <213> ORGANISM: Artificial Sequence
W--> 50 <220> FEATURE:
W--> 50 <223> OTHER INFORMATION:
      50 <400> SEQUENCE: 3
      51  ataatcgacg ttcaagcaag
      53 <210> SEQ ID NO: 4
      54 <211> LENGTH: 18
      55 <212> TYPE: DNA
      62 <213> ORGANISM: Artificial Sequence
W--> 64 <220> FEATURE:
W--> 64 <223> OTHER INFORMATION:
      64 <400> SEQUENCE: 4                                     18
      65  taccgcgtgc gaccctct
```

Does Not Comply
Corrected Diskette Needed
see pp. 1-5

<220>, <223> features mandatory with an artificial sequence. See #12 on Error Summary Sheet

RAW SEQUENCE LISTING   DATE: 10/03/2000
PATENT APPLICATION: US/09/669,187   TIME: 15:21:53

Input Set : A:\C10397035US.txt
Output Set: N:\CRF3\10032000\I669187.raw

```
     67 <210> SEQ ID NO: 5
     68 <211> LENGTH: 9
     69 <212> TYPE: DNA
     70 <213> ORGANISM: Artificial Sequence
W--> 72 <220> FEATURE:
W--> 72 <223> OTHER INFORMATION:
     72 <400> SEQUENCE: 5                                          9
     73  ggggagggt
     75 <210> SEQ ID NO: 6
     76 <211> LENGTH: 9
     77 <212> TYPE: DNA
     78 <213> ORGANISM: Artificial Sequence
W--> 80 <220> FEATURE:
W--> 80 <223> OTHER INFORMATION:
     80 <400> SEQUENCE: 6                                          9
     81  ggggaggggg
     83 <210> SEQ ID NO: 7
     84 <211> LENGTH: 9
     85 <212> TYPE: DNA
     86 <213> ORGANISM: Artificial Sequence
W--> 88 <220> FEATURE:
W--> 88 <223> OTHER INFORMATION:
     88 <400> SEQUENCE: 7                                          9
     89  ggtgaggtg
     91 <210> SEQ ID NO: 8
     92 <211> LENGTH: 20
     93 <212> TYPE: DNA
     94 <213> ORGANISM: Artificial Sequence
     96 <220> FEATURE:
     97 <221> NAME/KEY: modified_base
     98 <222> LOCATION: (8)...(8)
     99 <223> OTHER INFORMATION: m5c
    101 <400> SEQUENCE: 8                                          20
W--> 102  tccatgtngt tcctgatgct
    104 <210> SEQ ID NO: 9
    105 <211> LENGTH: 15
    106 <212> TYPE: DNA
    107 <213> ORGANISM: Artificial Sequence
    109 <220> FEATURE:
    110 <221> NAME/KEY: modified_base
    111 <222> LOCATION: (11)...(11)
    112 <223> OTHER INFORMATION: m5c
    114 <400> SEQUENCE: 9                                          15
W--> 115  gctaccttag ngtga
    117 <210> SEQ ID NO: 10
    118 <211> LENGTH: 20
    119 <212> TYPE: DNA
    120 <213> ORGANISM: Artificial Sequence
    122 <220> FEATURE:
```

[Handwritten annotation: refer to p.1]

[Handwritten annotation: no <220>, <223> feature to explain artificial sequence.]

```
       123 <221> NAME/KEY: modified_base
       124 <222> LOCATION: (8)...(8)
       125 <223> OTHER INFORMATION: m5c
       127 <400> SEQUENCE: 10                                    20
W--> 128  tccatgangt tcctgatgct
       130 <210> SEQ ID NO: 11
       131 <211> LENGTH: 20
       132 <212> TYPE: DNA
       133 <213> ORGANISM: Artificial Sequence   ───>   no <220>, <223> features
       135 <220> FEATURE:
       136 <221> NAME/KEY: modified_base
       137 <222> LOCATION: (13)...(13)
       138 <223> OTHER INFORMATION: m5c
       140 <400> SEQUENCE: 11                                    20
W--> 141  tccatgacgt tcntgatgct
       143 <210> SEQ ID NO: 12
       144 <211> LENGTH: 15
       145 <212> TYPE: DNA
       146 <213> ORGANISM: Artificial Sequence
       148 <220> FEATURE:
       149 <221> NAME/KEY: modified_base
       150 <222> LOCATION: (7)...(7)
       151 <223> OTHER INFORMATION: m5c
       153 <400> SEQUENCE: 12                                    15
W--> 154  gctagangtt agtgt
       156 <210> SEQ ID NO: 13
       157 <211> LENGTH: 19
       158 <212> TYPE: DNA
       159 <213> ORGANISM: Artificial Sequence
W--> 161 <220> FEATURE:
W--> 161 <223> OTHER INFORMATION:
       161 <400> SEQUENCE: 13                                    19
       162  agctccatgg tgctcactg
       164 <210> SEQ ID NO: 14
       165 <211> LENGTH: 20
       166 <212> TYPE: DNA
       167 <213> ORGANISM: Artificial Sequence
W--> 169 <220> FEATURE:
W--> 169 <223> OTHER INFORMATION:
       169 <400> SEQUENCE: 14
       170  ccacgtcgac cctcaggcga                                20
       172 <210> SEQ ID NO: 15
       173 <211> LENGTH: 20
       174 <212> TYPE: DNA
       175 <213> ORGANISM: Artificial Sequence
W--> 177 <220> FEATURE:
W--> 177 <223> OTHER INFORMATION:
       177 <400> SEQUENCE: 15                                    20
       178  gcacatcgtc ccgcagccga
```

Same as above

```
180 <210> SEQ ID NO: 16
181 <211> LENGTH: 19
182 <212> TYPE: DNA
183 <213> ORGANISM: Artificial Sequence
185 <220> FEATURE:
185 <223> OTHER INFORMATION:
185 <400> SEQUENCE: 16                                    19
186  gtcactcgtg gtacctcga
188 <210> SEQ ID NO: 17
189 <211> LENGTH: 25
190 <212> TYPE: DNA
191 <213> ORGANISM: Artificial Sequence
193 <220> FEATURE:
193 <223> OTHER INFORMATION:
193 <400> SEQUENCE: 17                                    25
194  gttggataca ggccagactt tgttg
196 <210> SEQ ID NO: 18
197 <211> LENGTH: 25
198 <212> TYPE: DNA
199 <213> ORGANISM: Artificial Sequence
201 <220> FEATURE:
201 <223> OTHER INFORMATION:
201 <400> SEQUENCE: 18                                    25
202  gattcaactt gcgctcatct taggc
204 <210> SEQ ID NO: 19
205 <211> LENGTH: 24
206 <212> TYPE: DNA
207 <213> ORGANISM: Artificial Sequence
209 <220> FEATURE:
209 <223> OTHER INFORMATION:
209 <400> SEQUENCE: 19                                    24
210  accatggacg aactgtttcc cctc
212 <210> SEQ ID NO: 20
213 <211> LENGTH: 24
214 <212> TYPE: DNA
215 <213> ORGANISM: Artificial Sequence
217 <220> FEATURE:
217 <223> OTHER INFORMATION:
217 <400> SEQUENCE: 20                                    24
218  accatggacg agctgtttcc cctc
220 <210> SEQ ID NO: 21
221 <211> LENGTH: 24
222 <212> TYPE: DNA
223 <213> ORGANISM: Artificial Sequence
225 <220> FEATURE:
225 <223> OTHER INFORMATION:
225 <400> SEQUENCE: 21                                    24
226  accatggacg acctgtttcc cctc
228 <210> SEQ ID NO: 22
```

Same

```
229 <211> LENGTH: 24
230 <212> TYPE: DNA
231 <213> ORGANISM: Artificial Sequence
W--> 233 <220> FEATURE:
W--> 233 <223> OTHER INFORMATION:
233 <400> SEQUENCE: 22                                    24
234   accatggacg tactgtttcc cctc
236 <210> SEQ ID NO: 23
237 <211> LENGTH: 24
238 <212> TYPE: DNA
239 <213> ORGANISM: Artificial Sequence
W--> 241 <220> FEATURE:
W--> 241 <223> OTHER INFORMATION:
241 <400> SEQUENCE: 23                                    24
242   accatggacg gtctgtttcc cctc
244 <210> SEQ ID NO: 24
245 <211> LENGTH: 24
246 <212> TYPE: DNA
247 <213> ORGANISM: Artificial Sequence
W--> 249 <220> FEATURE:
W--> 249 <223> OTHER INFORMATION:
249 <400> SEQUENCE: 24                                    24
250   accatggacg ttctgtttcc cctc
252 <210> SEQ ID NO: 25
253 <211> LENGTH: 25
254 <212> TYPE: DNA
255 <213> ORGANISM: Artificial Sequence
W--> 257 <220> FEATURE:
W--> 257 <223> OTHER INFORMATION:
257 <400> SEQUENCE: 25                                    25
258   ccactcacat ctgctgctcc acaag
260 <210> SEQ ID NO: 26
261 <211> LENGTH: 25
262 <212> TYPE: DNA
263 <213> ORGANISM: Artificial Sequence
W--> 265 <220> FEATURE:
W--> 265 <223> OTHER INFORMATION:
265 <400> SEQUENCE: 26                                    25
266   acttctcata gtccctttgg tccag
268 <210> SEQ ID NO: 27
269 <211> LENGTH: 20
270 <212> TYPE: DNA
271 <213> ORGANISM: Artificial Sequence
W--> 273 <220> FEATURE:
W--> 273 <223> OTHER INFORMATION:
273 <400> SEQUENCE: 27                                    20
274   tccatgagct tcctgagtct
276 <210> SEQ ID NO: 28
277 <211> LENGTH: 20
```

Same

↙ F.Y.I.

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220> to
<223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY   DATE: 10/03/2000
PATENT APPLICATION: US/09/669,187   TIME: 15:21:54

Input Set : A:\C10397035US.txt
Output Set: N:\CRF3\10032000\I669187.raw

L:13 M:270 C: Current Application Number differs, Replaced Current Application No
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:42 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:42 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:50 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:50 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:64 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:64 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:72 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:72 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:80 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:80 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:88 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:88 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:102 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:115 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:128 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:141 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:154 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:161 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:161 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:169 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:169 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:177 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:177 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:185 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:185 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:193 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:193 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:201 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:201 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:209 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:209 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:217 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:217 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:225 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:225 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:233 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:233 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:241 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:241 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:249 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:249 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:257 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:257 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:265 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:265 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:273 M:258 W: Mandatory Feature missing, <220> FEATURE:

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/669,187

DATE: 10/03/2000
TIME: 15:21:54

Input Set : A:\C10397035US.txt
Output Set: N:\CRF3\10032000\I669187.raw

```
L:273 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:295 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
L:316 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29
L:323 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:323 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:331 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:331 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:339 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:339 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:347 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:347 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:473 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:48
L:802 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:88
L:815 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:89
L:1020 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:113
L:1553 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:179
L:1566 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:180
L:1916 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:222
L:2154 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:249
L:2183 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:251
L:2452 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:284
L:2489 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:288
L:2522 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:289
L:2659 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:304
L:2745 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:313
L:2931 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:335
L:2948 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:336
L:2961 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:337
L:2974 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:338
L:3122 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:354
L:3171 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:358
L:3644 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:414
L:5946 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:698
L:6023 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:707
L:6044 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:709
L:6057 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:710
L:6211 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:728
L:6224 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:729
L:6237 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:730
L:6250 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:731
L:6263 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:732
L:6502 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:760
L:6523 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:762
L:6536 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:763
L:6557 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:764
L:6863 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:798
L:6888 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:800
L:6905 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:801
L:6922 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:802
```

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/669,187

DATE: 10/03/2000
TIME: 15:21:54

Input Set : A:\C10397035US.txt
Output Set: N:\CRF3\10032000\I669187.raw

L:6939 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:803
L:8571 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1001
L:8880 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1039
L:9025 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1056